



SEQUENCE LISTING

<110> Simmons, Laura

<120> METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
CULTURE

<130> 11669.120USU1

<140> US 10/764,428

<141> 2004-01-23

<150> US 60/442,484

<151> 2003-01-23

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> FR1 SGI

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 2

<211> 25

<212> PRT

<213> Artificial Sequence

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<223> FR1 SGII

<400> 2

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 3

<211> 25

<212> PRT

<213> Artificial Sequence

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<223> FR1 SGIII

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 4

<211> 3300

<212> DNA

<213> Artificial Sequence

<220>

<223> pxVG11VNERK

<400> 4

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<210> 5
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> The first 214 amino acids are the light chain followed by the heavy chain beginning at position 215 (E).

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Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly
210 215 220

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
225 230 235 240

Tyr Thr Phe Thr Asn Tyr Gly Ile Asn Trp Val Arg Gln Ala Pro Gly
245 250 255

Lys Gly Leu Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro
260 265 270

Thr Tyr Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr
275 280 285

Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
290 295 300

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Val Asn Glu
305 310 315 320

Arg Lys Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val
325 330 335

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
340 345 350

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
355 360 365

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
370 375 380

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 385 390 395 400

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 405 410 415

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 420 425 430

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 435 440 445

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 565 570 575

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 610 615 620

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 660 665 670

<210> 6
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 <212> DNA
 <213> Artificial Sequence

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 <223> pxVG2AP11

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 cgacgatacg gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300
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<210> 7
 <211> 667
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain begins at residue 1 (D); Heavy chain begins at
 residue 215 (E)

<400> 7

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 210 215 220
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 225 230 235 240
 Tyr Asp Phe Thr His Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly
 245 250 255
 Lys Gly Leu Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro
 260 265 270
 Thr Tyr Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr
 275 280 285
 Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 290 295 300
 Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr Ser
 305 310 315 320
 His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 325 330 335
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 340 345 350
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 355 360 365
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 370 375 380

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 385 390 395 400

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 405 410 415

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 420 425 430

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 435 440 445

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 450 455 460

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 465 470 475 480

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 485 490 495

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 500 505 510

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 515 520 525

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 530 535 540

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 545 550 555 560

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 565 570 575

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 580 585 590

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 595 600 605

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 610 615 620

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 625 630 635 640

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 645 650 655

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 660 665

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pVKFR1-2

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tagtcgcttt gtttttattt tttaatgtat ttgtaactag tacgcaagtt cacgtaaaaa	1560
gggtatctag aattatgaag aagaatatcg catttcttct tgcattctatg ttcgtttttt	1620
ctattgctac aaacgcgtac gctcagggttc agctgggtgca gtctggcgca gaggtgaaaa	1680
agccaggggc ttcagttaaa gtatcctgta aagcttctgg ctataccttc accaactatg	1740
gtataaactg ggtccgtcag gccccgggta agggcctgga atgggttggga tggattaaca	1800
cctataccgg tgaaccgacc tatgctgcgg atttcaaacg tcgtttcact ttttcttttag	1860
acacctccaa aagcacagca tacctgcaga tgaacagcct gcgcgctgag gacactgccg	1920
tctattactg tgcaaagtac ccgcactatt atgtgaacga gcggaagagc cactggtatt	1980
tcgacgtctg ggggtcaagga accctgggtca ccgtctctc ggccctccacc aagggcccat	2040
cggctctccc cctggcacc tctccaaga gcacctctgg gggcacagcg gccctgggct	2100
gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca ggcgccctga	2160
ccagcggcgt gcacaccttc ccggctgtcc tacagtctc aggactctac tccctcagca	2220
gcgtggtgac tgtgccctct agcagcttgg gcacccagac ctacatctgc aacgtgaatc	2280
acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt gacaaaactc	2340
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tcttctctca cagcaagctc accgtggaca agagcagggtg gcagcagggg aacgtcttct	2940
catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc ctctccctgt	3000

ctccgggtaa ataagcatgc gacggcccta gaggccctaa cgctcgggtg ccgccgggcg 3060
 ttttttattg ttaactcatg ttgacagct tatcatcgat aagctttaat gcggtagttt 3120
 atcacagtta aattgctaac gcagtcaggc accgtgtatg aaatctaaca atgcgctcat 3180
 cgtcatcctc ggcaccgtca ccctgggatgc tgtaggcata ggcttggtta tgccggtact 3240
 gccgggcctc ttgcgggata tcgtccattc cgacagcatc gccagtcact atggcgtgct 3300

<210> 9
 <211> 670
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain starts at residue 1 (D); Heavy chain starts at
 residue 215 (Q)

<400> 9

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145		150		155		160
Glu Ser Val Thr	Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser					
	165			170		175
Ser Thr Leu Thr	Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr					
	180		185			190
Ala Cys Glu Val	Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser					
	195		200			205
Phe Asn Arg Gly	Glu Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu					
	210		215			220
Val Lys Lys Pro	Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly					
	225		230		235	240
Tyr Thr Phe Thr	Asn Tyr Gly Ile Asn Trp Val Arg Gln Ala Pro Gly					
	245		250			255
Lys Gly Leu Glu	Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro					
	260		265			270
Thr Tyr Ala Ala	Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr					
	275		280			285
Ser Lys Ser Thr	Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp					
	290		295			300
Thr Ala Val Tyr	Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Val Asn Glu					
	305		310		315	320
Arg Lys Ser His	Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val					
	325		330			335
Thr Val Ser Ser	Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala					
	340		345			350
Pro Ser Ser Lys	Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu					
	355		360			365
Val Lys Asp Tyr	Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly					
	370		375		380	
Ala Leu Thr Ser	Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser					

385		390		395		400									
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
				405					410					415	
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr
			420					425					430		
Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
		435					440					445			
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
	450					455					460				
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
465					470					475					480
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
				485					490					495	
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
			500					505					510		
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
		515					520					525			
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
	530					535					540				
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
545					550					555					560
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
				565					570					575	
Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
			580					585					590		
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
		595					600					605			
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
	610					615					620				
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp

640

17

ctcgggttgcc gccggggcggt ttttattgtt gccgacgcgc atctcgaatg aactgtgtgc	1260
gcaggtagaa gctttggaga ttatcgtcac tgcaatgctt cgcaatatgg cgcaaaatga	1320
ccaacagcgg ttgattgatc aggtagaggg ggcgctgtac gaggtaaagc ccgatgccag	1380
cattcctgac gacgatacgg agctgctgcg cgattacgta aagaagttat tgaagcatcc	1440
tcgtcagtaa aaagttaatc ttttcaacag ctgtcataaa gttgtcacgg ccgagactta	1500
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gggtatctag aattatgaag aagaatatcg catttcttct tgcattctatg ttcgtttttt	1620
ctattgctac aaacgcgtac gctcagggtc agctgcaaga gtctggcccc ggctgggtga	1680
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gtataaactg ggtccgctcag gccccgggta agggcctgga atgggttgga tggattaaca	1800
cctataccgg tgaaccgacc tatgctgcgg atttcaaacg tcgtttcact ttttctttag	1860
acacctcaa aagcacagca tacctgcaga tgaacagcct gcgcgctgag gacactgccg	1920
tctattactg tgcaaagtac ccgcactatt atgtgaacga gcggaagagc cactgggtatt	1980
tcgacgtctg gggtaagga accctgggtc ccgtctcctc ggcctccacc aagggcccat	2040
cggctcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg gccctgggct	2100
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ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac tccctcagca	2220
gcgtgggtgac tgtgccctct agcagcttgg gcaccagac ctacatctgc aacgtgaatc	2280
acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt gacaaaactc	2340
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ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg	2460
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gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag tgcaaggctc	2640
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gagaaccaca ggtgtacacc ctgcccccat cccgggaaga gatgaccaag aaccagggtca	2760
gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag tgggagagca	2820
atgggcagcc ggagaacaac tacaagacca cgctccccgt gctggactcc gacggctcct	2880
tcttctcta cagcaagctc accgtggaca agagcagggtg gcagcagggg aacgtcttct	2940
catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc ctctccctgt	3000

ctccgggtaa ataagcatgc gacggcccta gaggccctaa cgctcgggtg ccgccgggcg 3060
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 cgtcatcctc ggcaccgtca ccctggatgc tgtaggcata ggcttggtta tgccggtact 3240
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<210> 11
 <211> 670
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain starts at residue 1 (D); Heavy chain starts at
 residue 215 (Q)

<400> 11

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
210 215 220

Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
225 230 235 240

Tyr Thr Phe Thr Asn Tyr Gly Ile Asn Trp Val Arg Gln Ala Pro Gly
245 250 255

Lys Gly Leu Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro
260 265 270

Thr Tyr Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr
275 280 285

Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
290 295 300

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Val Asn Glu
305 310 315 320

Arg Lys Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val
325 330 335

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
340 345 350

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
355 360 365

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
370 375 380

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
385 390 395 400

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
405 410 415

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
420 425 430

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
435 440 445

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
565 570 575

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
610 615 620

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 12
<211> 3300
<212> DNA
<213> Artificial Sequence

<220>
<223> pYOFR1-2

<400> 12
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agctttggag attatcgtca ctgcaatgct tcgcaatatg gcgcaaaatg accaacagcg 180
gttgattgat caggtagagg gggcgctgta cgaggtaaag cccgatgcca gcattcctga 240
cgacgatacg gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300
aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt atagtcgctt 360
tggtttttatt ttttaatgta tttgtaacta gtacgcaagt tcacgtaaaa agggatatcta 420
gaattatgaa gaagaatatt gcattttcttc ttgcatctat gttcgttttt tctattgcta 480
caaacgcgta cgctgatatt cagttgacct agtccccgag ctccctgtcc gcctctgtgg 540
gcgatagggg caccatcacc tgcagcgcaa gtcaggatat tagcaactat ttaaactggg 600
atcaacagaa accaggaaaa gctccgaaag tactgattta cttcacctcc tctctccact 660
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gcagtctgca gccagaagac ttcgcaactt attactgtca acagtatagc accgtgccgt 780
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tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac gccctccaat 960
cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc tacagcctca 1020
gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac gcctgcgaag 1080
tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga gagtgttaat 1140
taaattcctt acgccggacg catcgtggcg agctcggtag ccgggggatct aggcctaacg 1200
ctcgggtgcc gccgggaggt ttttattgtt gccgacgcgc atctcgaatg aactgtgtgc 1260

gcaggtagaa	gctttggaga	ttatcgtcac	tgcaatgctt	cgcaatatgg	cgcaaaatga	1320
ccaacagcgg	ttgattgac	aggtagaggg	ggcgctgtac	gaggtaaagc	ccgatgccag	1380
cattcctgac	gacgatacgg	agctgctgcg	cgattacgta	aagaagttat	tgaagcatcc	1440
tcgtcagtaa	aaagttaatc	ttttcaacag	ctgtcataaa	gttgtcacgg	ccgagactta	1500
tagtcgcttt	gtttttat	tttaatgtat	ttgtaactag	tacgcaagtt	cacgtaaaaa	1560
gggtatctag	aattatgaag	aagaatatcg	catttcttct	tgcacttatg	ttcgtttttt	1620
ctattgctac	aaacgcgtac	gctcagggtc	agctgggtgca	gtctggcgca	gaggtgaaaa	1680
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aggactactt	ccccgaaccg	gtgacgggtg	cgtggaactc	aggcgccctg	accagcggcg	2160
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aggtgtacac	cctgccccca	tcccgggaag	agatgaccaa	gaaccagggtc	agcctgacct	2760
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tgatgcatga	ggctctgcac	aaccactaca	cgcagaagag	cctctccctg	tctccgggta	3000
aataagcatg	cgacggccct	agagtcccta	acgctcgggt	gccgcccggc	gttttttatt	3060

gttaactcat gtttgacagc ttatcatcga taagctttaa tgcggtagtt tatcacagtt 3120
 aaattgctaa cgcagtcagg caccgtgtat gaaatctaac aatgcgctca tcgtcatcct 3180
 cggcaccgtc accctggatg ctgtaggcat aggcttggtt atgccggtac tgccgggcct 3240
 cttgcgggat atcgccatt ccgacagcat cgccagtcac tatggcgtgc tgctagcgct 3300

<210> 13
 <211> 667
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain starts at residue 1 (D); Heavy chain starts at
 residue 215 (Q)

<400> 13

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu
 210 215 220

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 225 230 235 240

Tyr Asp Phe Thr His Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly
 245 250 255

Lys Gly Leu Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro
 260 265 270

Thr Tyr Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr
 275 280 285

Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 290 295 300

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr Ser
 305 310 315 320

His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 325 330 335

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 340 345 350

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 355 360 365

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 370 375 380

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 385 390 395 400

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 405 410 415
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 420 425 430
 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 435 440 445
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 450 455 460
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 465 470 475 480
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 485 490 495
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 500 505 510
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 515 520 525
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 530 535 540
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 545 550 555 560
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 565 570 575
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 580 585 590
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 595 600 605
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 610 615 620
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 625 630 635 640

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
645 650 655

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR1 residues 26-35

<400> 14

Gly Tyr Thr Phe Thr Asn Tyr Gly Ile Asn
1 5 10

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SGI consensus sequence

<400> 15

Gly Tyr Thr Phe Thr Ser Tyr Ala Ile Ser
1 5 10

<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SGII consensus sequence

<400> 16

Gly Gly Ser Val Ser Ser Tyr Trp Ser Trp Asn
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SGIII consensus sequence

<400> 17

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
 1 5 10

<210> 18
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YO317 VH HVR1 residues 26-35

<400> 18

Gly Tyr Asp Phe Thr His Tyr Gly Met Asn
 1 5 10

<210> 19
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> E25 VH HVR1 residues 26-35

<400> 19

Gly Tyr Ser Ile Thr Ser Gly Tyr Ser Trp Asn
 1 5 10

<210> 20
 <211> 3300
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> E25 in pE25-11

<400> 20
 gaattcaact tctccatact ttggataagg aaatacagac atgaaaaatc tcattgctga 60
 gttgttattt aagcttgccc aaaaagaaga agagtcgaat gaactgtgtg cgcaggtaga 120
 agctttggag attatcgta ctgcaatgct tcgcaatatg gcgcaaaatg accaacagcg 180
 gttgattgat caggtagagg gggcgctgta cgaggtaaag cccgatgccg gcattcctga 240
 cgacgatacg gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300
 aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt atagtcgctt 360
 tgtttttatt ttttaatgta tttgtaacta gtacgcaagt tcacgtaaaa agggatatcta 420
 gaattatgaa gaagaatatc gcatttcctt ttgcatctat gttcgttttt tctattgcta 480
 caaacgcgta cgctgatatc cagctgaccc agtccccgag ctccctgtcc gcctctgtgg 540

gcgatagggg	caccatcacc	tgccgtgcc	gtcagagcgt	cgattacgat	ggtgatagct	600
acatgaactg	gtatcaacag	aaaccaggaa	aagctccgaa	actactgatt	tacgcggcct	660
cgtacctgga	gtctggagtc	ccttctcgct	tctctggatc	cggttctggg	acggatttca	720
ctctgaccat	cagcagtctg	cagccggaag	acttcgcaac	ttattactgt	cagcaaagtc	780
acgaggatcc	gtacacattt	ggacagggtg	ccaagggtga	gatcaaacga	actgtggctg	840
caccatctgt	cttcatcttc	ccgccatctg	atgagcagtt	gaaatctgga	actgcctctg	900
ttgtgtgcct	gctgaataac	ttctatccca	gagaggccaa	agtacagtgg	aagggtggata	960
acgccctcca	atcgggtaac	tcccaggaga	gtgtcacaga	gcaggacagc	aaggacagca	1020
cctacagcct	cagcagcacc	ctgacgctga	gcaaagcaga	ctacgagaaa	cacaaagtct	1080
acgcctgcga	agtcacccat	cagggcctga	gctcgcccg	cacaaagagc	ttcaacaggg	1140
gagagtgtta	attaaatcct	ctacgccgga	cgcatcgctg	cgagctcggt	acccggggat	1200
ctaggcctaa	cgctcggttg	ccgccggg	ttttttattg	ttgccgacgc	gcatctcgaa	1260
tgaactgtgt	gcgcaggtag	aagctttgga	gattatcgct	actgcaatgc	ttcgcaatat	1320
ggcgcaaaat	gaccaacagc	ggttgattga	tcaggtagag	ggggcgctgt	acgaggtaaa	1380
gcccgatgcc	agcattcctg	acgacgatac	ggagctgctg	cgcgattacg	taaagaagtt	1440
attgaagcat	cctcgtcagt	aaaaagttaa	tcttttcaac	agctgtcata	aagttgtcac	1500
ggccgagact	tatagtcgct	ttgtttttat	tttttaatgt	atttgtaact	agtacgcaag	1560
ttcacgtaaa	aagggtatct	agaattatga	agaagaatat	cgcatcttct	cttgcatcta	1620
tgttcgtttt	ttctattgct	acaaacgcgt	acgctgaggt	tcagctggtg	gagtctggcg	1680
gtggcctggg	gcagccaggg	ggctcactcc	gtttgtcctg	tgagtttct	ggctactcca	1740
tcacctccgg	atatagctgg	aactggatcc	gtcaggcccc	gggtaagggc	ctggaatggg	1800
ttgcatcgat	tacgtatgac	ggatcgacta	actataaccc	tagcgtcaag	ggccgtatca	1860
ctataagtcg	cgacgactcc	aaaaacacat	tctacctgca	gatgaacagc	ctgcgtgctg	1920
aggacactgc	cgtctattat	tgtgctcgag	gcagccacta	tttcggtcac	tggcacttcg	1980
ccgtgtgggg	tcaaggaacc	ctggtcaccg	tctcctcggc	ctccaccaag	ggcccatcgg	2040
tcttccccct	ggcaccctcc	tccaagagca	cctctggggg	cacagcggcc	ctgggctgcc	2100
tgggtcaagga	ctacttcccc	gaaccgggtg	cggtgtcgctg	gaactcaggc	gccctgacca	2160
gcggcggtga	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	ctcagcagcg	2220
tgggtgactgt	gccctctagc	agcttgggca	cccagaccta	catctgcaac	gtgaatcaca	2280
agcccagcaa	caccaagggtg	gacaagaaa	ttgagcccaa	atcttgtgac	aaaactcaca	2340

catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc ctcttcccc 2400
caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc gtgggtgg 2460
acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc gtggaggtgc 2520
ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt gtggtcagcg 2580
tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc aaggtctcca 2640
acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg cagccccgag 2700
aaccacaggt gtacaccctg ccccatccc gggaagagat gaccaagaac caggtcagcc 2760
tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg gagagcaatg 2820
ggcagccgga gaacaactac aagaccacgc ctcccgctgt ggactccgac ggctccttct 2880
tcctctacag caagctcacc gtggacaaga gcagggtggca gcagggaac gtcttctcat 2940
gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc tccctgtctc 3000
cgggtaaata agcatgcgac ggccctagag tccctaacgc tcggttgccg ccgggcgttt 3060
tttattgtta actcatgttt gacagcttat catcgataag ctttaatgcg gtagtttatc 3120
acagttaa at tgctaacgca gtcaggcacc gtgtatgaaa tctaacaatg cgctcatcgt 3180
catcctcggc accgtcacc tggatgctgt aggcataaggc ttggttatgc cgg tactgcc 3240
gggcctcttg cgggatatcg tccattccga cagcatcgcc agtcactatg gcgtgctgct 3300

<210> 21

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain starts at residue 1 (D); Heavy chain starts at residue 220 (E)

<400> 21

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His
 85 90 95
 Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Glu Val Gln Leu Val Glu
 210 215 220
 Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 225 230 235 240
 Ala Val Ser Gly Tyr Ser Ile Thr Ser Gly Tyr Ser Trp Asn Trp Ile
 245 250 255
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile Thr Tyr
 260 265 270
 Asp Gly Ser Thr Asn Tyr Asn Pro Ser Val Lys Gly Arg Ile Thr Ile
 275 280 285
 Ser Arg Asp Asp Ser Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu
 290 295 300

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser His Tyr
 305 310 315 320

Phe Gly His Trp His Phe Ala Val Trp Gly Gln Gly Thr Leu Val Thr
 325 330 335

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 340 345 350

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 355 360 365

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 370 375 380

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 385 390 395 400

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 405 410 415

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 420 425 430

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 435 440 445

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 450 455 460

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 465 470 475 480

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 485 490 495

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 500 505 510

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 515 520 525

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 530 535 540

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
545 550 555 560

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
565 570 575

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
580 585 590

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
595 600 605

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
610 615 620

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
625 630 635 640

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
645 650 655

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 22
<211> 3300
<212> DNA
<213> Artificial Sequence

<220>
<223> E25 VH FR1 SGII in pE25-SGII

<400> 22
gaattcaact tctccatact ttggataagg aaatacagac atgaaaaatc tcattgctga 60
gttggttattt aagcttgccc aaaaagaaga agagtcgaat gaactgtgtg cgcaggtaga 120
agctttggag attatcgtca ctgcaatgct tcgcaatatg gcgcaaaatg accaacagcg 180
gttgattgat caggtagagg gggcgctgta cgaggtaaag cccgatgcca gcattcctga 240
cgacgatacg gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300
aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt atagtcgctt 360
tgtttttatt ttttaatgta tttgtaacta gtacgcaagt tcacgtaaaa agggtatcta 420
gaattatgaa gaagaatatc gcatttcttc ttgcatctat gttcgttttt tctattgcta 480
caaacgcgta cgctgatatc cagctgaccc agtccccgag ctccctgtcc gcctctgtgg 540
gcgatagggt caccatcacc tgccgtgcca gtcagagcgt cgattacgat ggtgatagct 600

acatgaactg gtatcaacag aaaccaggaa aagctccgaa actactgatt tacgcggcct	660
cgtacctgga gtctggagtc ccttctcgct tctctggatc cggttctggg acggatttca	720
ctctgaccat cagcagtctg cagccggaag acttcgcaac ttattactgt cagcaaagtc	780
acgaggatcc gtacacattt ggacagggta ccaaggtgga gatcaaacga actgtggctg	840
caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga actgcctctg	900
ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg aaggtggata	960
acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc aaggacagca	1020
cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct	1080
acgcctgcga agtcacccat cagggcctga gctcgccgt cacaaagagc ttcaacaggg	1140
gagagtgtta attaaatcct ctacgccgga cgcctcgtgg cgagctcggg acccggggat	1200
ctaggcctaa cgctcggttg ccgccgggcg ttttttattg ttgccgacgc gcatctcgaa	1260
tgaactgtgt gcgcaggtag aagctttgga gattatcgtc actgcaatgc ttcgcaatat	1320
ggcgcaaaat gaccaacagc ggttgattga tcaggtagag ggggcgctgt acgaggtaaa	1380
gcccgatgcc agcattcctg acgacgatac ggagctgctg cgcgattacg taaagaagtt	1440
attgaagcat cctcgtcagt aaaaagttaa tcttttcaac agctgtcata aagttgtcac	1500
ggccgagact tatagtcgct ttgtttttat tttttaatgt atttgtaact agtacgcaag	1560
ttcacgtaaa aagggtatct agaattatga agaagaatat cgcattttctt cttgcatcta	1620
tgttcgtttt ttctattgct acaaacgcgt acgctcaggt tcagctgcaa gagtctggcc	1680
cgggcctggg gaaaccatct cagactctct ccttgacttg tactgtttct ggctactcca	1740
tcacctccgg atatagctgg aactggatcc gtcaggcccc gggtaagggc ctggaatggg	1800
ttgcatcgat tacgtatgac ggatcgacta actataacct tagcgtcaag ggccgtatca	1860
ctataagtcg cgacgactcc aaaaacacat tctacctgca gatgaacagc ctgcgtgctg	1920
aggacactgc cgtctattat tgtgctcgag gcagccacta tttcggtcac tggcacttcg	1980
ccgtgtgggg tcaaggaacc ctggtcaccg tctcctcggc ctccaccaag ggccatcgg	2040
tcttccccct ggcacctcc tccaagagca cctctggggg cacagcggcc ctgggctgcc	2100
tggtcaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc gccctgacca	2160
gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc ctcagcagcg	2220
tggtgactgt gccctctagc agcttgggca ccagaccta catctgcaac gtgaatcaca	2280
agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac aaaactcaca	2340
catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc ctcttcccc	2400

caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc gtggtggtgg 2460
 acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc gtggaggtgc 2520
 ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt gtggtcagcg 2580
 tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc aaggtctcca 2640
 acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg cagccccgag 2700
 aaccacaggt gtacaccctg ccccatccc gggaagagat gaccaagaac caggtcagcc 2760
 tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg gagagcaatg 2820
 ggcagccgga gaacaactac aagaccacgc ctcccgctgt ggactccgac ggctccttct 2880
 tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac gtcttctcat 2940
 gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc tcctgtctc 3000
 cgggtaaata agcatgcgac ggccctagag tccctaacgc tcggttgccg ccgggcgttt 3060
 ttattgtta actcatgttt gacagcttat catcgataag ctttaatgcy gtagtttatc 3120
 acagttaa at tgctaacgca gtcaggcacc gtgtatgaaa tctaacaatg cgctcatcgt 3180
 catcctcggc accgtcacc tggatgctgt aggcataaggc ttggttatgc cgggtactgcc 3240
 gggcctcttg cgggatatcg tccattccga cagcatcgcc agtcactatg gcgtgctgct 3300

<210> 23
 <211> 669
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain starts at residue 1 (D); Heavy chain starts at
 residue 220 (Q)

<400> 23

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 35

65		70		75		80									
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	His
				85					90					95	
Glu	Asp	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105					110		
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
		115					120					125			
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
	130					135					140				
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
145					150					155					160
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
			165						170					175	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
		180						185					190		
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
		195					200					205			
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	Gln	Val	Gln	Leu	Gln	Glu
	210					215					220				
Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys
225					230					235					240
Thr	Val	Ser	Gly	Tyr	Ser	Ile	Thr	Ser	Gly	Tyr	Ser	Trp	Asn	Trp	Ile
			245						250					255	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Ser	Ile	Thr	Tyr
			260					265					270		
Asp	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Val	Lys	Gly	Arg	Ile	Thr	Ile
		275					280					285			
Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Phe	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	290					295					300				
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Ser	His	Tyr

305		310		315		320
Phe Gly His Trp	His 325	Phe Ala Val Trp	Gly 330	Gln Gly Thr	Leu Val Thr	335
Val Ser Ser	Ala 340	Ser Thr Lys Gly	Pro 345	Ser Val Phe Pro	Leu Ala Pro	350
Ser Ser	Lys 355	Ser Thr Ser Gly	Gly 360	Thr Ala Ala Leu	Gly Cys Leu Val	365
Lys Asp Tyr Phe	Pro Glu Pro	Val Thr Val	Ser Trp	Asn Ser Gly Ala		
	370		375		380	
Leu Thr Ser Gly	Val His Thr	Phe Pro Ala	Val Leu Gln	Ser Ser Gly		
385		390		395		400
Leu Tyr Ser	Leu Ser Ser	Val Val Thr	Val Pro Ser	Ser Ser Ser	Leu Gly	
	405		410		415	
Thr Gln Thr Tyr	Ile Cys Asn	Val Asn His	Lys Pro Ser	Asn Thr Lys		
	420		425		430	
Val Asp Lys Lys	Val Glu Pro	Lys Ser Cys	Asp Lys Thr	His Thr Cys		
	435		440		445	
Pro Pro Cys Pro	Ala Pro Glu	Leu Leu Gly	Gly Pro Ser	Val Phe Leu		
	450		455		460	
Phe Pro Pro Lys	Pro Lys Asp	Thr Leu Met	Ile Ser Arg	Thr Pro Glu		
465		470		475		480
Val Thr Cys Val	Val Val Asp	Val Ser His	Glu Asp Pro	Glu Val Lys		
	485		490		495	
Phe Asn Trp Tyr	Val Asp Gly	Val Glu Val	His Asn Ala	Lys Thr Lys		
	500		505		510	
Pro Arg Glu Glu	Gln Tyr Asn	Ser Thr Tyr	Arg Val Val	Ser Val Leu		
	515		520		525	
Thr Val Leu His	Gln Asp Trp	Leu Asn Gly	Lys Glu Tyr	Lys Cys Lys		
	530		535		540	
Val Ser Asn Lys	Ala Leu Pro	Ala Pro Ile	Glu Lys Thr	Ile Ser Lys		

545		550		555		560									
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
				565					570					575	
Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
			580					585					590		
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
		595					600					605			
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
	610					615					620				
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
625					630					635					640
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
				645					650					655	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
			660					665							

<210> 24
 <211> 3300
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pVG50

<400> 24	
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gttgattgat caggtagagg gggcgctgta cgaggtaaag cccgatgcca gcattcctga	240
cgacgatacg gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta	300
aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt atagtcgctt	360
tgtttttatt ttttaatgta tttgtaacta gtacgcaagt tcacgtaaaa agggtatcta	420
gaattatgaa gaagaatatc gcatttcctt ttgcatctat gttcgttttt tctattgcta	480
caaacgcgta cgctgatatc cagatgaccc agtccccgag ctccctgtcc gcctctgtgg	540
gcgatagggt caccatcacc tgcagcgcaa gtcaggatat tagcaactat ttaaactggt	600

atcaacagaa accaggaaaa gctccgaaag tactgattta cttcacctcc tctctccact	660
ctggagtccc ttctcgcttc tctggatccg gttctgggac ggatttcact ctgaccatca	720
gcagtctgca gccagaagac ttcgcaactt attactgtca acagtatagc accgtgccgt	780
ggacgttttg acaggggtacc aagggtggaga tcaaacgaac tgtggctgca ccatctgtct	840
tcattctccc gccatctgat gagcagttga aatctggaac tgcttctgtt gtgtgcctgc	900
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cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc tacagcctca	1020
gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac gcctgcgaag	1080
tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga gagtgttaat	1140
taaatcctct acgccggacg catcgtggcg agctcggtag ccggggatct aggcctaacg	1200
ctcggttgcc gccgggcgtt ttttattgtt gccgacgcgc atctcgaatg aactgtgtgc	1260
gcaggtagaa gctttggaga ttatcgtcac tgcaatgctt cgcaatatgg cgcaaaatga	1320
ccaacagcgg ttgattgatc aggtagaggg ggcgctgtac gaggtaaagc ccgatgccag	1380
cattcctgac gacgatacgg agctgctgcg cgattacgta aagaagtat tgaagcatcc	1440
tcgtcagtaa aaagttaatc ttttcaacag ctgtcataaa gttgtcacgg ccgagactta	1500
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ctattgctac aaacgcgtac gctgaggttc agctggtgga gtctggcggg ggcttgggtgc	1680
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cctataccgg tgaaccgacc tatgctgcgg atttcaaacg tcgtttcact ttcagcttag	1860
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ctgtgcctc tagcagcttg ggcacccaga cctacatctg caacgtgaat cacaagccca	2280
gcaacaccaa ggtggacaag aaagttgagc ccaaactctg tgacaaaact cacacatgcc	2340
caccgtgccc agcacctgaa ctcttggggg gaccgtcagt cttcctcttc ccccaaaaac	2400

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aaattgctaa cgcagtcagg caccgtgtat gaaatctaac aatgcgctca tcgtcatcct 3180
cggcaccgtc accctggatg ctgtaggcat aggcttggtt atgccggtac tgccgggcct 3240
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<210> 25

<211> 667

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain starts at residue 1 (D); Heavy chain starts at residue 215 (E)

<400> 25

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

```

```

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
          35           40           45

```

```

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```


His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 325 330 335

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 340 345 350

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 355 360 365

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 370 375 380

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 385 390 395 400

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 405 410 415

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 420 425 430

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 435 440 445

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 450 455 460

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 465 470 475 480

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 485 490 495

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 500 505 510

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 515 520 525

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 530 535 540

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 545 550 555 560

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
565 570 575

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
580 585 590

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
595 600 605

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
610 615 620

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
625 630 635 640

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
645 650 655

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 26
<211> 3300
<212> DNA
<213> Artificial Sequence

<220>
<223> pVKSGI with FR1-4 SGI consensus sequence

<400> 26
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gttgattgat caggtagagg gggcgcgtga cgaggtaaag cccgatgcca gcattcctga 240
cgacgatacg gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300
aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt atagtcgctt 360
tgttttttatt ttttaagtga tttgtaacta gtacgcaagt tcacgtaaaa agggatatcta 420
gaattatgaa gaagaatatc gcatttcttc ttgcatctat gttcgttttt tctattgcta 480
caaacgcgta cgctgatatc cagttgaccc agtccccgag ctccctgtcc gcctctgtgg 540
gcgatagggt caccatcacc tgcagcgcaa gtcaggatat tagcaactat ttaaactggg 600
atcaacagaa accaggaaaa gctccgaaag tactgattta cttcacctcc tctctccact 660

ctggagtccc	ttctcgcttc	tctggatccg	gttctgggac	ggatttcact	ctgaccatca	720
gcagtctgca	gccagaagac	ttcgcaactt	attactgtca	acagtatagc	accgtgccgt	780
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tcattcttccc	gccatctgat	gagcagttga	aatctggaac	tgcttctgtt	gtgtgcctgc	900
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cgggtaactc	ccaggagagt	gtcacagagc	aggacagcaa	ggacagcacc	tacagcctca	1020
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tcacccatca	gggcctgagc	tcgcccgtca	caaagagctt	caacagggga	gagtgttaat	1140
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ctcggttgcc	gccgggcggt	ttttattgtt	gccgacgcgc	atctcgaatg	aactgtgtgc	1260
gcaggtagaa	gctttggaga	ttatcgtcac	tgcaatgctt	cgcaatatgg	cgcaaaatga	1320
ccaacagcgg	ttgattgatc	aggtagaggg	ggcgctgtac	gaggtaaagc	ccgatgccag	1380
cattcctgac	gacgatacgg	agctgctgcg	cgattacgta	aagaagttat	tgaagcatcc	1440
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<210> 27

<211> 670

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain starts at residue 1 (D); Heavy chain starts at residue 215 (Q)

<400> 27

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu
 210 215 220

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 225 230 235 240

Tyr Thr Phe Thr Asn Tyr Gly Ile Asn Trp Val Arg Gln Ala Pro Gly
 245 250 255

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro
 260 265 270

Thr Tyr Ala Ala Asp Phe Lys Arg Arg Val Thr Ile Thr Ala Asp Thr
 275 280 285

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
 290 295 300

Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Pro His Tyr Tyr Val Asn Glu
 305 310 315 320

Arg Lys Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val
325 330 335

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
340 345 350

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
355 360 365

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
370 375 380

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
385 390 395 400

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
405 410 415

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
420 425 430

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
435 440 445

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
450 455 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465 470 475 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
485 490 495

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
500 505 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
515 520 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
530 535 540

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
545 550 555 560

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
565 570 575

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
580 585 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
595 600 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
610 615 620

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625 630 635 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
645 650 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 28
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> VH FR2 SGIII

<400> 28

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 29
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> VH FR2 VNERK

<400> 29

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

<210> 30
<211> 32
<212> PRT

<213> Artificial Sequence

<220>

<223> VH FR3 SGI III

<400> 30

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 31

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> VH FR3 VNERK

<400> 31

Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
20 25 30

<210> 32

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> VH FR4 SGI III

<400> 32

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 33

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> VH FR3 SGI

<400> 33

Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30